

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Dana-Farber, Corporation  
KOLODNER, Richard  
WINAND, Nena
- (ii) TITLE OF THE INVENTION: A Method for Detection of Alteration in MSH5
- (iii) NUMBER OF SEQUENCES: 104
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
(B) STREET: 130 Water Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/051,686  
(B) FILING DATE: 03-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Eisenstein, Ronald I  
(B) REGISTRATION NUMBER: 30,628  
(C) REFERENCE/DOCKET NUMBER: 157/47483-PCT
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617-523-3400  
(B) TELEFAX: 617-523-6440  
(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCTCCCTTT	GCAGGGCTCGT	GGCGGTCGGT	CAGCGGGCG	TTCTCCCACC	TGTAGCGACT	60
CAGGTTACTG	AAAAGGCGGG	AAAACGCTGC	GATGGCGCA	GCTGGGGGAG	GAGGAAGATA	120
AGCGCGTGAG	GCTGGGGTCC	TGGCGCGTGG	TTGGCAGAGG	CAGAGACATA	AGACGTGCAC	180
GACTCGCCCC	ACAGGGCCTT	CAGACCCCTT	CTTTCACAAAG	GAGCCTCCAA	GCTCATGGCC	240
TCCTTAGGAG	CGAACCCAAG	GAGGACACCG	CAGGGACCGA	GACCTGGGGC	GGCCTCCTCC	300
GGTTTCCCCA	GCCCGGCCCC	AGTGCCGGGC	CCCAGGGAGG	CCGAGGAGGA	GGAAAGTCGAG	360
GAGGAGGAGG	AGCTGGCCGA	GATCCATCTG	TGTGTGCTGT	GGAATTCAAGG	ATACTTGGC	420
ATTGCCTACT	ATGATACTAG	TGACTCCACT	ATCCACTTCA	TGCCAGATGC	CCCAGACCAC	480
GAGAGCCTCA	AGCTTCTCCA	GAGAGTTCTG	GATGAGATCA	ATCCCCAGTC	TGTTGTTACG	540
AGTGCCAAAC	AGGATGAGAA	TATGACTCGA	TTTCTGGAA	AGCTTGCCTC	CCAGGAGCAC	600
AGAGAGCCTA	AAAGACCTGA	AATCATATT	TTGCCAACGT	TGGATTTGG	TCTGGAGATA	660
AGCAAACAAAC	GCCTCCTTTC	TGGAAAATAC	TCCTTCATCC	CAGACGCCAT	GAUTGCCACT	720
GAGAAAATCC	TCTTCCTCTC	TTCCATTATT	CCCTTGTACT	GCCTCCTCAC	AGTTCGAGCA	780
CTTGGAGGGC	TGCTGAAGTT	CCTGGGTCGA	AGAAGAACG	GGGTTGAAC	GGAAAGACTAT	840
AATGTCAGCG	TCCCCATCCT	GGGCTTTAAG	AAATTTATGT	TGACTCATCT	GGTGAACATA	900
GATCAAGACA	CTTACAGTGT	TCTACAGATT	TTTAAGAGTG	AGTCTCACCC	CTCAGTGTAC	960
AAAGTGGCCA	GTGGACTGAA	GGAGGGGCTC	AGCCTTTTG	GAATCCTCAA	CAGATGCCAC	1020
TGTAAGTGGG	GAGAGAACG	GCTCAGGCTA	TGGTTCACAC	GTCCGACTCA	TGACCTGGGG	1080
GAGCTCAGTT	CTCGTCTGGA	CGTCATTCA	TTTTTCTGC	TGCCCCAGAA	TCTGGACATG	1140
GCTCAGATGC	TGCATCGGCT	CCTGGGTAC	ATCAAGAACG	TGCTTTGAT	TCTGAAACGC	1200
ATGAAGTTGT	CCCACACCAA	GGTCAGCGAC	TGGCAGGTT	TCTACAAGAC	TGTGTACAGT	1260
GCCCTGGGCC	TGAGGGATGC	CTGCCGCTCC	CTGCCGCACT	CCATCCAGCT	CTTTCGGGAC	1320
ATTGCCCAAG	AGTTCTCTGA	TGACCTGCAC	CATATGCCA	GCCTCATTGG	AAAAGTAGTG	1380
GACTTTGAGG	GCAGCCTTGC	TGAAAATCGC	TTCACAGTC	TCCCCAACAT	AGATCCTGAA	1440
ATTGATGAGA	AAAAGCGAAG	ACTGATGGGA	CTTCCCAGTT	TCCTTACTGA	GGTTGCCCGC	1500
AAGGAGCTGG	AGAATCTGGA	CTCCCGTATT	CCTTCATGCA	GTGTCATCTA	CATCCCTCTG	1560
ATTGGCTTCC	TTCTTTCTAT	TCCCCGCCTG	CCTTCCATGG	TAGAGGCCAG	TGACTTTGAG	1620
ATTAATGGAC	TGGACTTCAT	GTTCCTCTCA	GAGGAGAACG	TGCACTATCG	TAGTGCCGA	1680
ACCAAGGAGC	TGGATGCATT	GCTGGGGGAC	CTGCACTGCG	AGATCCGGGA	CCAGGAGACG	1740
CTGCTGATGT	ACCAGCTACA	GTGCCAGGTG	CTGGCAGAG	CAGCTGTCTT	AACCCGAGTA	1800
TTGGACCTTG	CCTCCCGCCT	GGACGTCTG	CTGGCTCTG	CCAGTGTGTC	CCGGGACTAT	1860
GGCTACTCAA	GGCGCGCTTA	CTCCCCACAA	GTCCTTGGGG	TACGAATCCA	GAATGGCAGA	1920
CATCCCTCTGA	TGGAACTCTG	TGCCCCAAC	TTTGTGCCCA	ACTCCACAGA	ATGTGGTGGG	1980
GACAAAGGGA	GGGTCAAAGT	CATCACTGGA	CCCAACTCAT	CAGGGAAGAG	CATATACCTC	2040
AAACAGGTAG	GCTTGATCAC	ATTCACTGCC	CTGGTAGGCA	GCTTTGTGCC	AGCAGAGGAG	2100
GCCGAAATTG	GGGCAGTAGA	CGCCATCTC	ACACGAATT	ATAGCTGC	ATCCCATCTCC	2160
CTTGGCCTCT	CCACCTTCAT	GATCGACCTC	AACCAGGTGG	CGAAAGCAGT	GAACAATGCC	2220
ACTGCACAGT	CGCTGGTCCT	TATTGATGAA	TTTGGAAAGG	GAACCAACAC	GGTGGATGGG	2280
CTCGCGCTTC	TGGCGCGTGT	GCTCCGACAC	TGGCTGGCAC	GTGGACCCAC	ATGCCCTCAC	2340
ATCTTTGTGG	CCACCAAATT	TCTGAGCCTT	GTTCACTAC	AACTGCTGCC	ACAAGGGCCC	2400
CTGGTGCAGT	ATTTGACCAT	GGAGACCTGT	GAGGATGGCA	ACGATCTGT	CTTCTCTAT	2460
CAGGTTTGCG	AAGGTGTGTC	GAAGGCCAGC	CATGCCCTCC	ACACAGCTGC	CCAGGCTGGG	2520
CTTCTGACA	AGCTTGTGGC	TCGTGGCAAG	GAGGTCTCAG	ATTGATCCG	CAGTGGAAAA	2580
CCCATCAAGC	CTGTCAAGGA	TTTGTAAAG	AAGAACAAA	TGGAAAATTG	CCAGACATTA	2640

B9470E376 422239

GTGGATAAGT TTATGAAACT GGATTTGAA GATCCTAACCC TGGACTTGAA CGTTTCATG	2700
AGCCAGGAAG TGCTGCCTGC TGCCACCAGC ATCCTCTGAG AGTCCTTCCA GTGTCCTCCC	2760
CAGCCTCCTG AGACTCCGGT GGGCTGCCAT GCCCTCTTG TTTCTTATC TCCCTCAGAC	2820
GCAGAGTTTT TAGTTTCTCT AGAAATTTG TTTCATATTA GGAATAAAGT TTATTTGAA	2880
GAAAAAAA AAAAAAAA	2900

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Leu Gly Ala Asn Pro Arg Arg Thr Pro Gln Gly Pro Arg			
1	5	10	15
Pro Gly Ala Ala Ser Ser Gly Phe Pro Ser Pro Ala Pro Val Pro Gly			
20	25	30	
Pro Arg Glu Ala Glu Glu Glu Val Glu Glu Glu Glu Leu Ala			
35	40	45	
Glu Ile His Leu Cys Val Leu Trp Asn Ser Gly Tyr Leu Gly Ile Ala			
50	55	60	
Tyr Tyr Asp Thr Ser Asp Ser Thr Ile His Phe Met Pro Asp Ala Pro			
65	70	75	80
Asp His Glu Ser Leu Lys Leu Leu Gln Arg Val Leu Asp Glu Ile Asn			
85	90	95	
Pro Gln Ser Val Val Thr Ser Ala Lys Gln Asp Glu Asn Met Thr Arg			
100	105	110	
Phe Leu Gly Lys Leu Ala Ser Gln Glu His Arg Glu Pro Lys Arg Pro			
115	120	125	
Glu Ile Ile Phe Leu Pro Ser Val Asp Phe Gly Leu Glu Ile Ser Lys			
130	135	140	
Gln Arg Leu Leu Ser Gly Asn Tyr Ser Phe Ile Pro Asp Ala Met Thr			
145	150	155	160
Ala Thr Glu Lys Ile Leu Phe Leu Ser Ser Ile Ile Pro Phe Asp Cys			
165	170	175	
Leu Leu Thr Val Arg Ala Leu Gly Gly Leu Leu Lys Phe Leu Gly Arg			
180	185	190	
Arg Arg Ile Gly Val Glu Leu Glu Asp Tyr Asn Val Ser Val Pro Ile			
195	200	205	
Leu Gly Phe Lys Lys Phe Met Leu Thr His Leu Val Asn Ile Asp Gln			
210	215	220	
Asp Thr Tyr Ser Val Leu Gln Ile Phe Lys Ser Glu Ser His Pro Ser			
225	230	235	240
Val Tyr Lys Val Ala Ser Gly Leu Lys Glu Gly Leu Ser Leu Phe Gly			
245	250	255	
Ile Leu Asn Arg Cys His Cys Lys Trp Gly Glu Lys Leu Leu Arg Leu			
260	265	270	
Trp Phe Thr Arg Pro Thr His Asp Leu Gly Glu Leu Ser Ser Arg Leu			
275	280	285	

Asp Val Ile Gln Phe Phe Leu Leu Pro Gln Asn Leu Asp Met Ala Gln  
 290 295 300  
 Met Leu His Arg Leu Leu Gly His Ile Lys Asn Val Pro Leu Ile Leu  
 305 310 315 320  
 Lys Arg Met Lys Leu Ser His Thr Lys Val Ser Asp Trp Gln Val Leu  
 325 330 335  
 Tyr Lys Thr Val Tyr Ser Ala Leu Gly Leu Arg Asp Ala Cys Arg Ser  
 340 345 350  
 Leu Pro Gln Ser Ile Gln Leu Phe Arg Asp Ile Ala Gln Glu Phe Ser  
 355 360 365  
 Asp Asp Leu His His Ile Ala Ser Leu Ile Gly Lys Val Val Asp Phe  
 370 375 380  
 Glu Gly Ser Leu Ala Glu Asn Arg Phe Thr Val Leu Pro Asn Ile Asp  
 385 390 395 400  
 Pro Glu Ile Asp Glu Lys Lys Arg Arg Leu Met Gly Leu Pro Ser Phe  
 405 410 415  
 Leu Thr Glu Val Ala Arg Lys Glu Leu Glu Asn Leu Asp Ser Arg Ile  
 420 425 430  
 Pro Ser Cys Ser Val Ile Tyr Ile Pro Leu Ile Gly Phe Leu Leu Ser  
 435 440 445  
 Ile Pro Arg Leu Pro Ser Met Val Glu Ala Ser Asp Phe Glu Ile Asn  
 450 455 460  
 Gly Leu Asp Phe Met Phe Leu Ser Glu Glu Lys Leu His Tyr Arg Ser  
 465 470 475 480  
 Ala Arg Thr Lys Glu Leu Asp Ala Leu Leu Gly Asp Leu His Cys Glu  
 485 490 495  
 Ile Arg Asp Gln Glu Thr Leu Leu Met Tyr Gln Leu Gln Cys Gln Val  
 500 505 510  
 Leu Ala Arg Ala Ala Val Leu Thr Arg Val Leu Asp Leu Ala Ser Arg  
 515 520 525  
 Leu Asp Val Leu Ala Leu Ala Ser Ala Ala Arg Asp Tyr Gly Tyr  
 530 535 540  
 Ser Arg Pro Arg Tyr Ser Pro Gln Val Leu Gly Val Arg Ile Gln Asn  
 545 550 555 560  
 Gly Arg His Pro Leu Met Glu Leu Cys Ala Arg Thr Phe Val Pro Asn  
 565 570 575  
 Ser Thr Glu Cys Gly Gly Asp Lys Gly Arg Val Lys Val Ile Thr Gly  
 580 585 590  
 Pro Asn Ser Ser Gly Lys Ser Ile Tyr Leu Lys Gln Val Gly Leu Ile  
 595 600 605  
 Thr Phe Met Ala Leu Val Gly Ser Phe Val Pro Ala Glu Glu Ala Glu  
 610 615 620  
 Ile Gly Ala Val Asp Ala Ile Phe Thr Arg Ile His Ser Cys Glu Ser  
 625 630 635 640  
 Ile Ser Leu Gly Leu Ser Thr Phe Met Ile Asp Leu Asn Gln Val Ala  
 645 650 655  
 Lys Ala Val Asn Asn Ala Thr Ala Gln Ser Leu Val Leu Ile Asp Glu  
 660 665 670  
 Phe Gly Lys Gly Thr Asn Thr Val Asp Gly Leu Ala Leu Leu Ala Ala  
 675 680 685  
 Val Leu Arg His Trp Leu Ala Arg Gly Pro Thr Cys Pro His Ile Phe  
 690 695 700  
 Val Ala Thr Asn Phe Leu Ser Leu Val Gln Leu Leu Pro Gln

705	710	715	720
Gly Pro Leu Val Gln Tyr Leu Thr Met Glu Thr Cys Glu Asp Gly Asn			
725		730	735
Asp Leu Val Phe Phe Tyr Gln Val Cys Glu Gly Val Ala Lys Ala Ser			
740	745	750	
His Ala Ser His Thr Ala Ala Gln Ala Gly Leu Pro Asp Lys Leu Val			
755	760	765	
Ala Arg Gly Lys Glu Val Ser Asp Leu Ile Arg Ser Gly Lys Pro Ile			
770	775	780	
Lys Pro Val Lys Asp Leu Leu Lys Lys Asn Gln Met Glu Asn Cys Gln			
785	790	795	800
Thr Leu Val Asp Lys Phe Met Lys Leu Asp Leu Glu Asp Pro Asn Leu			
805	810	815	
Asp Leu Asn Val Phe Met Ser Gln Glu Val Leu Pro Ala Ala Thr Ser			
820	825	830	
Ile Leu			

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCAAAGGG TAACCTCCGC GTGACAGAA  
29

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGCCGAGG TCTCTGAGGG GAGTAGAAA

29

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCAGAGAGG TGGGGATGGA ACCATGAAT

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAAGCTTGG TAAGGACTTG GTAAAGGAT

29

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGGATTTGG TATCTCCTTC CTTTTGCTT

29

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCTCACAG TGAGATTGGT CCTGGGGGA

29

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATTTATGTTG TAGGTGATTC ACCCCAACC

29

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACTTACAGG TAAAGAGGTG GAGGCATGC

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTCTTGG TAGGTGTGCC CCATCCCTC

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGCTCAGG TGAGTGGTC CCACACATA

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACGTGCCTG TGAGCCCAGG GTGGAGGGC

29

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTACAAGG TAAGGCCTTC CTTCTTGAA

29

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGAAAGTAG TGAGTAGAAG GAAAAAGGG

29

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGATGAGAG TGAGTGTGG GTGTGGATG

29

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCCCTCTGG TGAGGGCAGG AGAGTGGGT

29

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GACTTCATGG TAAGACCCTC AACCTCTGT

29

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGATCCGGGG TGAGGAAAAG CCAGAGGTT

29

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATGGCAGG TAAGAATAGA GGCGGGTGG

29

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCAAACAGG TGAGGAGAAG CCCTGCAGC

29

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCAACCAGG TCAAAGGGAA CAAAGGGAG

29

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCAACACGG TGAGGGGAGA AACTGATGA

29

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGTATTTGG TGAGGGAGACC AATCTAGCT

29

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCAAGGAGG TGATGAGATC CAAATGTGC

29

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATGGAAAAG TCGGTATATG GCCCCAGTG

29

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCACTTTGCATCCGCAG AGCCTCCAA

29

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTTTCTTCCT TGCTGGACAG ATCCATCTG

29

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTCTGTT CTCCTTCCAG TTCTGGATG

29

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTTCTTCC TCCCCCACAG CCTCCCAGG

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGCTTGCCTC CCTCAAATAG GTCTGGAGA

29

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CACTGCTGAT CCCCTCCCAG GTTCGAGCA

29

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTTTGTTTT CTGTCCTCAG GACTCATCT

29

(2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCTCCATTTC TCCTCGACAG TGTTCTACA

29

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTGCCTTAT CCCTCACAAAG AATCCTCAA

29

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACCCAAACCC TCACTTCCAG GCTATGGTT

29

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTAACCTTGT CTGACTGTAG TTGATTCTG

29

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTGTGTT TCTCTCACAG ACTGTGTAC

29

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGTACTT ATCTCCTCAG GTGGACTTT

29

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTGTCTTCC ACCCTCGTAG AAAAGCGAA

29

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCCTCTTTA CTCTCCCCAG ATTGGCTTC

29

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTGAACCC CTGTACCCAG TTTCTCTCA

29

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCTTCCTCAC CCACTCCCAG ACCAGGAGA

29

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGCCTCTCCG CCCACTGCAG ACATCCTCT

29

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGTCTCCTT CCCTATTCAAG GTAGGCTTG

29

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTCCACCTTA TACCCAGCAG GTGGCGAAA

29

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AACCTCTGCC CTCTTGCAG GTGGATGGG

29

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTCTTTTATT CTCTTTAAG ACCATGGAG

29

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CACCTTCTTG CTTGTCCTAG GTCTCAGAT

29

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGATTTCTC TCTTCTTCAG TTGCCAGAC

29

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GAATGGCAGA CATCCTCTGA

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTATATGCT CTTCCCTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTTGGGGC GGTTGGTCAG GGAGGTGGAT CGTCGCGGCT GAGAGTCGCC GAGCCATGG	60
CTTTCAAGGC GACCCCAGGC CGGACGCCGC CGGGACCCGG ACCCAGATCC GGAATCCCCT	120
CAGCCAGCTT CCCCCAGCCCT CAGCCCCCAA TGGCGGGGCC TGGAGGTATC GAGGAAGAGG	180
ACGAGGAGGA GCCCGCCGAG ATCCATCTGT GCGTGCTGTG GAGCTCGGGA TACCTGGCA	240
TTGCTTACTA TGACACTAGT GACTCCACTA TCCACTTCAT GCCAGATGCC CCAGACCACG	300
AGAGCCTAAA GCTTCTCCAG AGAGTTCTGG ATGAAATCAA CCCCCAGTCT GTTGTACAA	360
GTGCAAACAA GGATGAGGCT ATGACTCGAT TTCTAGGGAA GCTTGCCTCT GAGGAGCACA	420
GAGAGCCAAA GGGACCTGAA ATCATACTTC TGCCAAGCGT GGATTTTGGT CCAGAGATAA	480
GCAAACAGCG TCTCCTTCC GGAAACTACT CCTTCATCTC AGACTCCATG ACTGCTACTG	540

AGAAAATCCT	TTTCCTCTCC	TCCATTATTTC	CCTTGACTG	TGTCCCTCACG	GTCCGGGCAC	6000
TTGGAGGACT	GCTCAAGTTC	CTGAGTCGAA	GAAGAATTGG	GGTTGAACTG	GAAGACTATG	6600
ATGTTGGCGT	CCCTATCCTG	GGATTCAAGA	AGTTTGTATT	GACCCATCTG	GTGAGCATAG	7200
ATCAAGACAC	TTACAGCGTT	CTACAGATT	TCAGAGTGA	GTCTCACCCC	TCGGTGTACA	7800
AAGTAGGCCAG	TGGGCTGAAG	GAGGGGCTCA	GCCTTTTG	AATCCTAAC	AGATGCCGCT	8400
GTAAGTGGGG	ACAGAACGCTG	CTCAGGCTGT	GGTTTACACG	TCCAACCAGG	GAGCTAAGGG	9000
AACTCAATT	CCGACTGGAT	GTCATTAGT	TCTTCTGTAT	GCCTCAGAAC	CTGGACATGG	9600
CCCAGATGCT	GCACCGACTC	CTGAGCCACA	TCAGAACATGT	GCCTCTGATT	CTGAAACGCA	10200
TGAAGTTGTC	CCACACCAAG	GTCAGTGACT	GGCAGGTCT	CTACAAGACT	GTGTACAGTG	10800
CTCTCGGCCT	GAGGGATGCC	TGCCGTTCTC	TGCCACAGTC	CATCCAGCTT	TTTCAGGACA	11400
TTGCCCAAGGA	GTTCCTCTGAC	GACCTGCATC	ACATTGCCAG	CCTCATCGGG	AAGGTGGTGG	12000
ACTTTGAGGA	AAGTCCTGCT	GAAAATCGCT	TCACAGTCCT	CCCTAACATA	GACCCGTACA	12600
TAGATGCCAA	GAAGCGAAGG	CTGATAGGGC	TTCCGAGCTT	CCTCACTGAA	GTTGCTCAGA	13200
AGGAGCTGGA	GAACCTGGAC	TCTCGCATCC	CCTCATGCA	TGTCACTAC	ATCCCTCTGA	13800
TTGGCTTCCT	TCTTCCATT	CCCCGCTTGC	CTTTCATGGT	GGAAGCTAGT	GACTTTGAGA	14400
TTGAGGGGCT	GGACTTCATG	TTTCTCTCAG	AGGACAAGCT	GCACTATCGT	AGCGCCCCGGA	15000
CCAAGGAGCT	GGACACGCTG	CTGGGAGACC	TGCACTGTGA	GATCCGGAC	CAGGAGACTC	15600
TGTTGATGTA	CCAGCTGCAG	TGCCAGGTGC	TGGCACGGGC	TTCGGTCTTG	ACTCGGGTAT	16200
TGGACCTTGC	CTCCCCGCTG	GACGTCTTGT	TGGCTCTTGC	CAGTGTGCC	CGGGACTACG	16800
GCTATTGAG	ACCGCATTAC	TCTCCCTGTA	TCCATGGAGT	ACGAATCAGG	AATGGCAGGC	17400
ATCCTCTGAT	GGAACTGTGT	GCACGAAACCT	TCGTGCCAA	CTCCACGGAC	TGTGGTGGGG	18000
ACCAGGGCAG	GGTCAAAGTC	ATCACTGGAC	CCAACTCCTC	AGGGAAAAGC	ATATATCTCA	18600
AGCAGGTAGG	CTTGATCACT	TTCATGGCCC	TGGTGGGCAG	TTTCGTGCC	GCAGAGGAGG	19200
CCGAGATTGG	GGTAATCGAC	GCCATCTTCA	CTCGAATTCA	CAGCTGCGAA	TCCATCTCCC	19800
TCGGCCTCTC	CACCTTCATG	ATTGATCTCA	ACCAGGTGGC	GAAAGCAGTG	AAACATGCCA	20400
CAGAGCACTC	GCTGGTCTG	ATCGATGAAT	TCGGGAAGGG	GACCAACTCG	GTGGATGGCC	21000
TGGCACTTCT	GGCTGCTGTG	CTCCGTCACT	GGCTTGCACT	GGGACCCAGC	TGCCCCCAGC	21600
TCTTTGTAGC	CACCAACTTC	CTGAGCCTTG	TTCACTGTCA	GCTGTGCCG	CAAGGACCCC	22200
TGGTGCAGTA	TTTGACCATG	GAGACTTGTG	AGGATGGGG	AGACCTTGTG	TTCTTCTACC	22800
AGCTTGCCA	AGGCGTCGCC	AGTGCAGCC	ACGGCCTCCCA	CACAGCGGCC	CAGGCTGGC	23400
TTCCCTGACCC	ACTCATGCT	CGTGGCAAAG	AGGTCTCAGA	CTTGATCCGC	AGTGGAAAC	24000
CCATCAAGGC	CACGAATGAG	CTTCTAAGGA	GAAACCAAAT	GGAAAATG	CAGGCACTGG	24600
TGGATAAGTT	TCTAAAATG	GACITGGAGG	ATCCCCACCT	GGACCTGGAC	ATTTTCATTA	25200
GTCAGGAAGT	GCTGGCCCGCT	GCTCCACCA	TCCTCTGAGA	GTCCCTCCAG	TGTCTT	25760

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ala	Phe	Arg	Ala	Thr	Pro	Gly	Arg	Thr	Pro	Pro	Gly	Pro	Gly	Pro
1					5				10					15	
Arg	Ser	Gly	Ile	Pro	Ser	Ala	Ser	Phe	Pro	Ser	Pro	Gln	Pro	Pro	Met
								20					25		30
Ala	Gly	Pro	Gly	Gly	Ile	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Pro	Ala	Glu
								35					40		45
Ile	His	Leu	Cys	Val	Leu	Trp	Ser	Ser	Gly	Tyr	Leu	Gly	Ile	Ala	Tyr

50	55	60
Tyr Asp Thr Ser Asp Ser Thr Ile His Phe Met Pro Asp Ala Pro Asp		
65	70	75
His Glu Ser Leu Lys Leu Leu Gln Arg Val Leu Asp Glu Ile Asn Pro		80
85	90	95
Gln Ser Val Val Thr Ser Ala Lys Gln Asp Glu Ala Met Thr Arg Phe		
100	105	110
Leu Gly Lys Leu Ala Ser Glu Glu His Arg Glu Pro Lys Gly Pro Glu		
115	120	125
Ile Ile Leu Leu Pro Ser Val Asp Phe Gly Pro Glu Ile Ser Lys Gln		
130	135	140
Arg Leu Leu Ser Gly Asn Tyr Ser Phe Ile Ser Asp Ser Met Thr Ala		
145	150	155
Thr Glu Lys Ile Leu Phe Leu Ser Ser Ile Ile Pro Phe Asp Cys Val		160
165	170	175
Leu Thr Val Arg Ala Leu Gly Gly Leu Leu Lys Phe Leu Ser Arg Arg		
180	185	190
Arg Ile Gly Val Glu Leu Glu Asp Tyr Asp Val Gly Val Pro Ile Leu		
195	200	205
Gly Phe Lys Lys Phe Val Leu Thr His Leu Val Ser Ile Asp Gln Asp		
210	215	220
Thr Tyr Ser Val Leu Gln Ile Phe Lys Ser Glu Ser His Pro Ser Val		
225	230	235
Tyr Lys Val Ala Ser Gly Leu Lys Glu Gly Leu Ser Leu Phe Gly Ile		240
245	250	255
Leu Asn Arg Cys Arg Cys Lys Trp Gly Gln Lys Leu Leu Arg Leu Trp		
260	265	270
Phe Thr Arg Pro Thr Arg Glu Leu Arg Glu Leu Asn Ser Arg Leu Asp		
275	280	285
Val Ile Gln Phe Phe Leu Met Pro Gln Asn Leu Asp Met Ala Gln Met		
290	295	300
Leu His Arg Leu Leu Ser His Ile Lys Asn Val Pro Leu Ile Leu Lys		
305	310	315
Arg Met Lys Leu Ser His Thr Lys Val Ser Asp Trp Gln Val Leu Tyr		320
325	330	335
Lys Thr Val Tyr Ser Ala Leu Gly Leu Arg Asp Ala Cys Arg Ser Leu		
340	345	350
Pro Gln Ser Ile Gln Leu Phe Gln Asp Ile Ala Gln Glu Phe Ser Asp		
355	360	365
Asp Leu His His Ile Ala Ser Leu Ile Gly Lys Val Val Asp Phe Glu		
370	375	380
Glu Ser Leu Ala Glu Asn Arg Phe Thr Val Leu Pro Asn Ile Asp Pro		
385	390	395
Asp Ile Asp Ala Lys Lys Arg Arg Leu Ile Gly Leu Pro Ser Phe Leu		400
405	410	415
Thr Glu Val Ala Gln Lys Glu Leu Glu Asn Leu Asp Ser Arg Ile Pro		
420	425	430
Ser Cys Ser Val Ile Tyr Ile Pro Leu Ile Gly Phe Leu Leu Ser Ile		
435	440	445
Pro Arg Leu Pro Phe Met Val Glu Ala Ser Asp Phe Glu Ile Glu Gly		
450	455	460
Leu Asp Phe Met Phe Leu Ser Glu Asp Lys Leu His Tyr Arg Ser Ala		
465	470	475
		480

Arg Thr Lys Glu Leu Asp Thr Leu Leu Gly Asp Leu His Cys Glu Ile  
                   485                  490                  495  
 Arg Asp Gln Glu Thr Leu Leu Met Tyr Gln Leu Gln Cys Gln Val Leu  
                   500                  505                  510  
 Ala Arg Ala Ser Val Leu Thr Arg Val Leu Asp Leu Ala Ser Arg Leu  
                   515                  520                  525  
 Asp Val Leu Leu Ala Leu Ala Ser Ala Ala Arg Asp Tyr Gly Tyr Ser  
                   530                  535                  540  
 Arg Pro His Tyr Ser Pro Cys Ile His Gly Val Arg Ile Arg Asn Gly  
                   545                  550                  555                  560  
 Arg His Pro Leu Met Glu Leu Cys Ala Arg Thr Phe Val Pro Asn Ser  
                   565                  570                  575  
 Thr Asp Cys Gly Gly Asp Gln Gly Arg Val Lys Val Ile Thr Gly Pro  
                   580                  585                  590  
 Asn Ser Ser Gly Lys Ser Ile Tyr Leu Lys Gln Val Gly Leu Ile Thr  
                   595                  600                  605  
 Phe Met Ala Leu Val Gly Ser Phe Val Pro Ala Glu Glu Ala Glu Ile  
                   610                  615                  620  
 Gly Val Ile Asp Ala Ile Phe Thr Arg Ile His Ser Cys Glu Ser Ile  
                   625                  630                  635                  640  
 Ser Leu Gly Leu Ser Thr Phe Met Ile Asp Leu Asn Gln Val Ala Lys  
                   645                  650                  655  
 Ala Val Asn Asn Ala Thr Glu His Ser Leu Val Leu Ile Asp Glu Phe  
                   660                  665                  670  
 Gly Lys Gly Thr Asn Ser Val Asp Gly Leu Ala Leu Leu Ala Ala Val  
                   675                  680                  685  
 Leu Arg His Trp Leu Ala Leu Gly Pro Ser Cys Pro His Val Phe Val  
                   690                  695                  700  
 Ala Thr Asn Phe Leu Ser Leu Val Gln Leu Gln Leu Leu Pro Gln Gly  
                   705                  710                  715                  720  
 Pro Leu Val Gln Tyr Leu Thr Met Glu Thr Cys Glu Asp Gly Glu Asp  
                   725                  730                  735  
 Leu Val Phe Phe Tyr Gln Leu Cys Gln Gly Val Ala Ser Ala Ser His  
                   740                  745                  750  
 Ala Ser His Thr Ala Ala Gln Ala Gly Leu Pro Asp Pro Leu Ile Ala  
                   755                  760                  765  
 Arg Gly Lys Glu Val Ser Asp Leu Ile Arg Ser Gly Lys Pro Ile Lys  
                   770                  775                  780  
 Ala Thr Asn Glu Leu Leu Arg Arg Asn Gln Met Glu Asn Cys Gln Ala  
                   785                  790                  795                  800  
 Leu Val Asp Lys Phe Leu Lys Leu Asp Leu Glu Asp Pro Thr Leu Asp  
                   805                  810                  815  
 Leu Asp Ile Phe Ile Ser Gln Glu Val Leu Pro Ala Ala Pro Thr Ile  
                   820                  825                  830  
 Leu

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTAAACCTCCG CGTGACAGAA TGAGGGTGGG GCGCGTGGAG TTTCCCACAA TCTGTACTTT	60
AGTTAAATAC CCGAGAAATTC ACCTCCTGTG TCCACAGCTC TCCACGCCCG TCAGCCCTGC	120
CCCGCAGCCC TGTATCAGAA GTACTTAGCG CTTTGCATTC TGCGCGCCAC CCTACCCGG	180
CCTCCTCTGT GAATCGTTGC TTCCGAACCG CCCTCACTTT TTGCATCCGC AG	232

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTCTCTGAGG GGAGTAGAAA CTTGAATGGA GAGTTGATGG GAATTAAAAA TAAAAGAGGG	60
TTGGGAGCCG GG//	74

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AAAAAAAAAAC AGGGTTGGGA AGAGCTGGGC AAGTCTCTTA CCTCCTGAGT GGCTGTTCA	60
CATTCACTAA ATGGGGGTGA TGATGCCTAT CTCAGAGATT TGAGAAAATG ATTAAATTAT	120
ATAAGACATG GTAAACCTTA CACTTATGAG TGATTCTAAT AGTGATTTC CTTCTCCTT	180
GCTGGACAG	189

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTGGGGATGG AACCATGAAT TCCTCTGCTC TCTGGGATTG CAGATGTGTT ACACACACAC	60
ACACACACAC ACACACACAC ACACACATAT TTTTTTTTC TAGACAGAGT CTTGCTCTGT	120

TACCCAGGCT CAAGTGCAGT GGCGCAATCT TGGCTCACTG CAGCCTCCAC	CTCCTGGTT	180
CAAAGCAATT TCCTGACTCA ACCTCCCGAG TAGCTGGAC TACAGGCGTG	TGCCACCACA	240
CCCAGCTAGT TTTTGTGTG TGTTTTTAGC ACAGACGGTG TTTCACCATG	TTGGCCAGGG	300
TGGTCTAAA CTCTGACCT TGTGATCCGC CCACCTTGGC CTCCCTAAAGT	GCTGGGACTA	360
CAGGTGTGAG TCACCAAGCC CAGCCATGTT TTACTTACAT TAACTCACCT	CACTGTCTAG	420
CATATTTGTGTTGCTGTAA GGAAATAC//		450

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCGACAAAT ATATATGACG TATTTACAAT GTTTCAGGTG CTTCAGATTG AGCCCTGGC	60
AAATCAGTCA TGTCTGTTCT CCAGGGTTT ACAGCCTAGT GACAACATCC AGAACATCCC	120
ACTTCCCTCT CACCATCCCA CCACTCTTAA CTACTTTCT AAATCTCAAC TTCTACCTGT	180
GTTCCCCTG TGAGAGCAC TCCCTACTCC TAGGGAGGAA ATGTTTTGA GAAGGAGAGG	240
GGTAGGAAGA GGAGGGCTAT GGTTTTCTC TTAGTCAAAG ACAAAAGATCC TTTAACTCAT	300
TTGATCTCTG TTCTCCTTCC AAG	323

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTAAGGACTT GGTAAAGGAT AGAGGGAAAA TGGGGAAGGA CTAATATATG GAATATTCCA	60
GGGGGCTAGA ATTGGGTGAG AGGGAGTGTC AGACAGAGGT AGAAGGACTG AGATGTAAAG	120
AATGATAGCC TTTTCTTCC TCCCCCACAG	150

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 733 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTATCTCCTT CCTTTGCTT TGCCTAACTC CCTGTTCCGG TGTCCCATTC TTTCCCCCAA	60
CTCTACCTTC ATCATCACAG ATCTCCCCTC TGCCTTATGT CATCCTAAAC CTTTGTGCTC	120

CTCATGCCCT ATGACCTGTC CCCCAAGAT CTCTCCTGCT CCCTACCCCT TAATAATCTG	180
CAGCTTATTG GGAAGCCTCT GCTTAAGTCA TGTCTAGGGA TGAGGGCCTC CCCTGAGGAG	240
TGGTGACACT TTTTGGACAG GTTTTATTG TTGGAATTCT CCCCATTAAG TTAAAGCCTT	300
TTATCACCAA ACCAAAAGGC ACTGCCTCAG TGACCCCTAT TATGATCCAT AAGGCACCTC	360
TATAACTTTC CTAGGTTTAC AATAAGAACAA GGAGTGTACT ATCCTAATTA GATATTAAGG	420
CATTAGTGT ACTAGTTCTA TTAATACCAT TATTTTGACC AAAATCCTCA ATTCCAGACA	480
GATGTCTACT TTCCTCAGCC ATTATATCTT CTCAGGCTGT GCTTCAGAC AAGTATCTT	540
ATATTATATG TAGAATAAAA AGAGAATTAG ACTAAGAGTC TGAAAATTG GTTCTTGCTC	600
TAGCTTCCA TTAACTGCCT GTGTGAGCTT GGGCAAGTCA AATAATCTCT CTTGCTTCTA	660
TTGTCTCATT CTTAAAATGG GGTGAAAAAAA TTGAGCTACA AGACCGTTCC CTTTGCTTGC	720
CTCCCTCAAA TAG	733

## (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GTGAGATTGG TCCTGGGGGA TAAGGGCTGG GAGGCGGCAC AAGTGCTAGG GCTGAATTCT	60
GGGAGGTTACT GGCCTAGCCC TGGAAAATAG TAACTTTCCC TGGTGCTCTG CAGCCCCAG	120
GAGATTAAAG ATTTACCCCG ATTCCACTGC TGATCCCCTC CCAG	164

## (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTAGGTGATT CACCCCAACC CCAACCAAAG TAATGTGGGA TTGGGAGGCC TGAAAAGTAA	60
AGTGGGGGTG GGGTGTGGAT GTGGCTGTGA CCCAGTGGGT CAAGGGCTCT AGGACACCCG	120
GGAGAATCTA AGGGCTAATG AGACTTTGGG AAGAAGACTG GGACAATATT CAGAGAGGGG	180
GACAAAGGAA GTGGAGTTGT GGAACGAAC T CAGACTGCTT CCTGCTTTTG TGTTTCTGT	240
CCTCAG	246

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTAAAGAGGT GGAGGCATGC TGCTGTCTCT	GGGGAGGGAG AAGGATTAAG TTTAATGCC	60
CAATAATCCT AATGAGGCTC TAGTTTCCCT	AATCCTGGGG CTATTAAGAT CTCTCTCCTT	120
GAAGGAAAGG GAAGGGGGGT TTTGAGGGAA	AGAGAGGAAG AAAAGCATAA AGATACTAGC	180
TTTCTTTCT ATAGGGAGAA ACTGAGGCAA	AGAAAAGTAA GGGACAAACC TTACATCAAG	240
ATATGATCTC GGCTGGGC	GGTGGCTCAT GCCTGTAATC CCCCGCCTTT	300
GGCGGGTGG	GGGAGGCCAA TCAGGAGTTT GAGACCTGAC	360
TGCCTGAGG	CAATATGGTA AAACCCCGTC	
TCTACTAAAA ATATAAAAAT	TAGCTGGGTG TGTTGTGCGC CTGTAATCCC	413
	A//	

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTTTTTTTA AAAAAAAAAA AAAAAAGACG TGATCTCAGG AGGATATCCC CTGTCCCCAT	60
TCCATTATC AGTCCTCAAT TCTTATTCCC CTCAAAAGTC CAAGTTACCC CAAACTCCTC	120
CATTTCTCCT CGACAG	136

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTTAGGTGTGC CCCATCCCTC ATCTCACGTA CAAAGACCTA CCAGAAAAGC AATTGGCTCC	60
AAAGATGTGT CCCAGCCTCC CTTCCCACTT CACTCCCATT GTCAAGATATC TCTTTCATGC	120
CAATCCAAT TTCTTACCTA TTTGTACCCC CCGCCCCCA AGCTTGAGCA TCTTCCCATA	180
CTTTGTGGCT GTACAGTGTG TTGCAATATCA GCCATTACTT TACCAATTCT GTGTTCTTC	240
CCTGGGTTTG TATGAATGTT TCTACTAGTT GGGTACCTGT TAGGGACTTT GGGAGACCTT	300
GTGTATAGAG AAGAGTTTG TAACTGCATA ACTGCCTATT TGATTTGTAT AGAG//	356

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCAGGGAGTAG AGGGAGAGAC AGAAACAGCC AACAAATGGCC CAGAAAATGG ATGATATATT	60
AGATAAGGGA AGAAATGAGT TACCAGATTG GGGAGAGATG GTTGGATGT CAAAGCAGGT	120
GATCGGTGAC GTCAGCGTCC GAGGAAGAC GGCTGCCACC GGCGGGGCA GTTGAGGGAA	180
CTAGGTAGTT AAGTGTGTC GGGCTAAAAG TCCCTAGAGT GTCCCATCCCT CCCCCATCTC	240
CATGTGCGGT AATCCCAGCT CATTAGGGG CCAGGCACCA ACTTTGGTIG CCTTTGTGCC	300
CTCCCAGGCC AGCTTCCTCA ACAACCAGCA CCTCTGACTG GATGCCTCAG GTTAGACACA	360
TAAACACATT CCATTGCCCT GTCCGTGCCCT TGTAACAAGT TCACTCCCTG CCTTATCCCT	420
CACAAG	426

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTGAGTGGGT CCCACACATA CTACACACTA ATGCATGAAT TCCATATGCA CACTACATAC	60
TAAGCCTACT AATGGCAGTA TACAGATTCT CACATACACC ACCCCACCTA GTAGTAGTAA	120
AGCAACTGCC CTTTAAGTGGAG CACTGGCTAA CTGCATTCTCA TCCTTATAAC AGCTTTGTGT	180
AGTAGCTGAT ATGCATCTCA TTTTTGTTG TCAGCGCAGG TACACATATA CATTGATGAT	240
ACACAGACTT GCACACATAC AGCAGCAGGA AAAAACACAA AATGTAAGGC CGGGCACAGT	300
GGCTCACACC TGTTATCAGC ACTTTGGGGG GCCAACGCTG GGTGACCTTC CATTTTG//	360

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CACAGGAAGA ATATGAAAAG ATGAATGTCT GTTGCTGTTA CCCAGAGACA CTTTCACAGC	60
TAAAAAGACA TACAAACTCA TACTGACTCA CCGTCTCTTA CTCAGCCTCA GAGTGAGCTG	120
CAGTGGTGGC ACACAAATAC CTCAACACAC TGCTCTCCCT CTAAAATATT GACAAGCTCC	180
GTТАCTTATA TACATGGAAT GACACACGGT CTTATCCGTT GAAACTGTGA TATGTAGACA	240
CAATTATGCT CACATCTAGC AATTTTCAGT AGATACATGT AAACACACCT GAATGGGTAG	300
GACACTGCAC TTGCCACTAC ATTCCCATAG CACATCGTGG ATACATATTG CCACAATCCC	360
CAGGGACTGC AAGCACACTT TTTGGCAAAC TGAGATCAAG ATGATAGATG TAACTTGTAG	420
TACCCCCACC CAAACCCCTCA CTTCCAG	447

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTGAGCCCAG GGTGGAGGGC AGGGAGGTGG GGAAGGAGGT TGAGGGCTGA TACTGGCAG	60
TGGGCTTCTT GAGGGGCATT AGAGTGAGGG AAGAGAAAAC AGCGGCTGTA ACCTTGTCTG	120
ACTGTAG	127

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTAAGGCCTT CCTTCTTGAA TCCCCAAA//	30
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(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TACAGGCATG AGCCACTGTG CCTGCCAGG ACCATATCTT AATTGTCTTT GTAGTTTCAG	60
TGTTGGTAC AGTGCCTCTC ACTGTTCTT TTTGCCTTG AGATCTTCCC TCTTGTAC	120
TGTGATCTTC CCTACTGGTC TTTGTTCTTC TGAGTCTGTC CCTATCACCA CCTCAACCCG	180
AGCTGGATGT GGCCCTGTCTT CTTCTCTCAC AG	222

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTGAGTAGAA GGAAAAAGGG AGTGCACCCA GGGAGGTCAAG GGAGAGAGAA TGCAGTGTGC	60
AAGATGGGAA AACATGGAAG ATATTGAGGT CAATTGGATA AAGAATGGGA TGGTGGGAGG	120
AGGCAGCAGA ACTTCAGGGAA AGTATCTGGA GGGTGAGAGT TAAAGGAGGA CTGCAGGGAG	180

AATTGGGCC CAAGGAGAGC TGAGGAACAG GACAGAGGGT GCCAGGTCTT AAGAAACAGT      240  
 ACTTATCTCC TCAG      254

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGAGTGGTG GGTGTGGATG GGCTGTGAG CCCTGCGCAG TGATGGAGTA CCATCCTTGG      60  
 CAGGTGGTCA CCACAGCTGG GGATCTTCAT AGCAACCAGG GCAGGAGACT CACTTTGAT      120  
 AACCACCTGT CTTCCACCCCT CGTAG      145

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 98 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGAGGGCAG GAGAGTGGGT GTAGCCTTCA GATGTCTTTT GGGGGAGATA TTAGGCTTAT      60  
 GAAAGACATA CTGGTAGATA AGAAAACCTG TGGGC//      98

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATCTTTAAG CTCCCTGGG ATGGGGAGGT TCCAGTAAGT CTCCAAACAA GAGAGTAGAG      60  
 TATCTCCTCT TTACTCTCCC CAG      83

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTAAGACCCCT	CAACCTCTGT	AAGGTGAGTG	ATGAGGAAAAA	TGAGTCAGCA	GCTGAGGAAG	60
AGCGTTACTC	TACAGCAGCA	CTGCCAATA	TGGGATCTCT	CCTCTGTAGT	TTTACTCTGA	120
GCTTTACCAAG	CACTGAGACA	AAGGAAAGAG	AAGTCAGAGT	TAGGGGCTGG	AGGTGGGTT	180
AGAAAAGATGG	GGAAGGAGAG	GAGGACCAAG	AGATGCAAAG	TCCACAGCTT	TGAACCCCTG	240
TACCCAG						247

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGAGGAAAAA	GCCAGAGGTT	ATATGCATTG	TAAGATGTTT	AAAAAAAGCA	GCAGCCAGGG	60
GAAGGAGGGG	AGTGGGCAAC	TTGGGATGC	TTCCAACAGG	CCCCTCCTCT	TCCTGCTCTC	120
TGTCTCGCTC	ACTCTGACTC	TATCTTTCC	TCTGAATGTC	TTGAGGTCTC	AGATTGTATC	180
TGCAACCTGT	TTCCAGATCC	CCCTAGGGC	CTCTGCCTCT	CCTTCACTTT	CCCCCTGGAAC	240
TGACCTCCAG	CTCCCTTCCT	CACCACTCC	CAG			273

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTAAGAATAG	AGGCGGGTGG	AGGAATACAC	ATGAGGGGCC	CAAAGGCTAC	ATCTTCTGGG	60
GGTTCATCTA	TCTTGATCCA	CAAGCCATGC	GAGGTGCCTC	TCCGCCACT	GCAG	114

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTGAGGAGAA	GCCCTGCAGC	CTGGGCCTCT	GGCGTCTCCT	GCATCTACTC	CACCCCTACT	60
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TGCCAGCCAA	CTCAGGCTCC	TGCAGCTCTT	CTCCCATTTC	CTGACCCCGC	TCTTCATGAA	120
AGGACCATCA	CCCACATCCC	TGTGCTTCCA	CCTCACATGT	TCTTATTCTC	CACTGGAGAG	180
CCATGCTCTA	ATGGAACCTT	CCGTGGCCCA	AATTCCCTCA	CCTGCCTCTG	AGTAGGTACA	240
CACCACTCCC	AAGTATGTCT	CTGCCACGT	CCCGTGCCTC	TTCACTGATT	CTAAATTAGC	300
CCACAGGGCT	ATGGTCAGGA	TTCGGGGAGG	AGAGACAGAG	TCAGTGTGTC	TGTTACCTAT	360
TTCTCTGT	TCACCCTGTC	CATTCTCTT	TGATGTGCCA	TTCATGCCTT	GAGCCTCACT	420
TTCACCTCAG	CCCACGGCAC	CAGGCCAG	GCCCTGTCTC	CTTCCCTATT	CAG	473

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTCAAAGGGAA	ACAAAGGGAG	GTGGGATTGA	GGAAGGGGAT	AATGGGAAAG	GAACCCCTGA	60
AAATGCTCAT	ACAGGAAAG	CATGCCCTCT	GCTGCATGCC	CTTTATACTA	AAAGTGGGGA	120
GCACTAAGGT	CAGAGATAAG	AAGAATCAAT	ACCATAAACCA	TTTCTTGAAAC	CCTTGTTTCA	180
TGTGAGTCAC	TGTTGGCAAA	GAGGATGAAC	AAAGCGTGCA	CCTCACCATT	CAAGAACATTG	240
CAGTGCAGTA	GGGAGGGCAT	GTATACAGCT	TTATTACACAG	GCCAACGTG	GTCAGTGCCTG	300
TACGGGCTTC	CAATACTAAC	TTCCCTTGT	CCACCTTATA	CCCAGCAG		348

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GTGAGGGGAG	AAACTGATGA	GGGGAGAAC	TAAGGAGGGG	AAAATGGAGG	AGGATGAAGG	60
ACCATGACAG	TGAGGCTGGG	CCTCTGGAAT	GGAATAGGGC	TGTGTGGGCA	GAAAAGAAAT	120
AGAACACGAG	ACAGGGAAAG	GCAGTGCAAG	TGCAGAGGGG	CATATGGGGT	CCCCATGGCT	180
CCGAATGCTA	ACCTCTGCC	TCTTTGCAG				209

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTGAGGAGAC CAATCTAGCT CCTCGGGGAC CCCCAGGCTG GGCATTTCCC AGAGGTGGGG	60
ATTGGCTCCT CTATCAGAAC AAGGGCTCCC TCAGCACAGA GACCACATCC CTTCCCTTTT	120
CTCCCCCCC ACAGGATTGG CCAAGGGTTT CAGGACAGGA AGGAGGTGAT TGATGATACA	180
CTGTCTTTA TTCTCTTTA AG	202

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTGATGAGAT CCAAATGTGC AACCACCTCC ACATCAGAGC TCCCTTCAT TCCTAGTCCT	60
ACTGGGCCTG GGTCTAGGTC CACAGGATTG CTGACCCCTTA TTTCCCTTC TCTTCCCCAC	120
TCCCCCTTACT CCTCCCACCT TCTTGCTTGT CCTAG	155

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGCGTATAT GGCCCCAGTG TCTTTACCCCT CTCTGCATCT TCTCCTGCAA CTCTTCTCCC	60
CCCTCCAGCA CTTTGCCTT CAGAAACCCA CCATTTCTTT CTGAAATCCC TAAATCTTCA	120
AGATCCCAGG TTTTCTGTGC CACAGCCTCT CCCCTCTGCC CAGGGATTG GTTGTCCATT	180
CTGCCATAAAA TCTTGCGATT TTCTCTCTTC TTCAG	215

## (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCTGCTCAGG TATACAGTAC CACGCTCCC	29
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## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs

100

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGATCCGGGG TGAGGAGCCC GTGGTAGGA

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATGGCAGG TGAGAAGGGG CCCCCATGTC

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTCAAGCAGG TGAGGGGCCG CCAAGCTGG

29

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ACCAACTCGG TGCAGGAGGAA AATGAAGAG

29

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCCCATCCC AACCTCCAG GCTGTGGTT

29

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCTCTCTCT CCTTCTCCAG ACCAGGAGA

29

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTCTCTCTA CCCACCACAG GCATCCTCT

29

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTCCCCTGC CCTGGCCAG GTAGGCTTG

29

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCACCTCTGC CCTTGACAG GTGGATGGC

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTATACAGTA CCACGCTCCC CAAGCAAAGT CAAGATGAGA GAAGACGTGA CTTGTAACCT  
TCCCATCCCA ACCCTCCAG

60  
79

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTGAGGAGCC CGTGGTAGGA GGGGGCAGGC TGCTCTAACCA GACCCTGCTC TCATGCTGGC  
CCCTCTGCAT GGTACACTG CATCTGCATG CCTGCTTCCA GATCTTCCA GGCACCTCTC  
TCTCTCCTTC TCCAG

60  
120  
135

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGAGAAGGG GCCCCATGTC CTGCTGTGGG GATCCTCCCT GGGTCCACAA ACCATGCAGT  
GTCTCTCTAC CCACCACAG

60  
79

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGAGGGGCC	GCCAAGCTGG	GGGCCACAT	CTCCATCTCC	TCTGGCCGCC	AGGCCAGATC	60
CTCTGCCCCC	CCCCACACAC	ACATACAGCA	CATGTCCCTTG	TCCTCTGAGG	GACAGTCTGT	120
TCTTAGGAT	AGACCTTCC	GTGGCCACAA	GTCCCTGGAC	CAACCTCCAA	ATAGATCCAT	180
GCCGTTCCCT	AGTATGCCTT	TACCCACAAC	CTTGACTCTG	GAGTTAATTG	TGAAGTCAGG	240
ACCCAGGAAA	CTGTGTTCCA	GGGCTCTGTT	CTTCTGTTAC	ACTGTGTCCT	CTCTTTAAC	300
TGTCGTTCAT	GTCTTTAGTT	GAGACCCATT	TTTACTTTGC	CCATAGTACG	GCAACAGGCC	360
CATGTTCTGT	CTCCCCCTGCC	CTGGCCCGAG				389

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGCGGAGGA	AAATGAAGAG	ATGCTAAGGA	GGGGGGATGG	AGGAAAATGA	GAACCGGGAG	60
CAGGAGACTG	ACCTCAGGGA	AGAAAAGGGG	GATGCGTGCA	CAGAGGGGAG	GAGAAGCCAT	120
GACAGCTACA	GAAGGACACA	GCTGCTGG	TTCTGCCCTC	TCACCTCTGC	CCTTGACAG	180

## (2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CCAGAACTCT	CTGGAGAAC					20
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## (2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTGCTGTGGA ATTCAGGATA C

21

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTCCACTATC CACTTCATGC CAGATGC

27

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTGGGGAGG ACACGTGGAAAG GACTCTCA

28